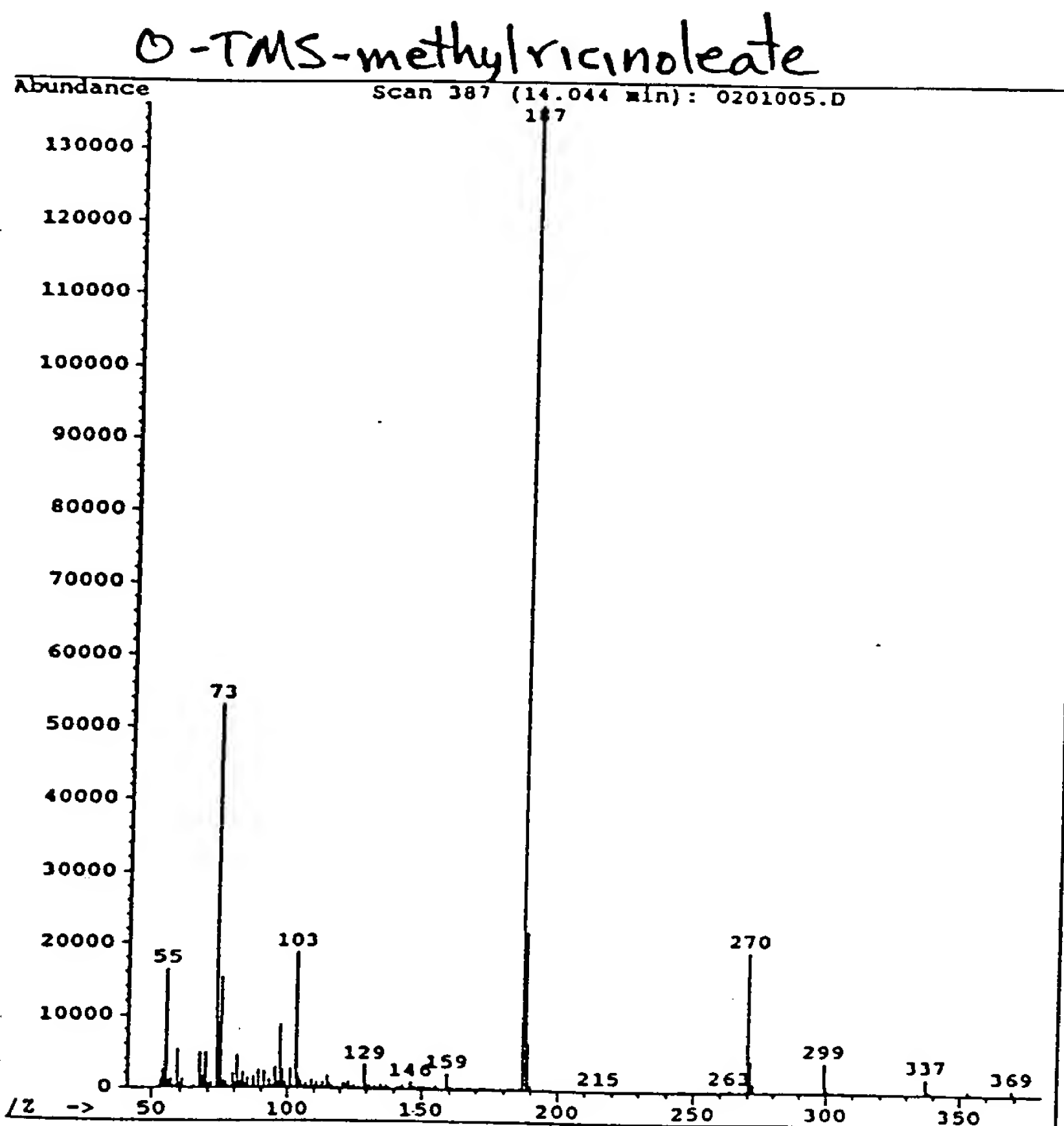
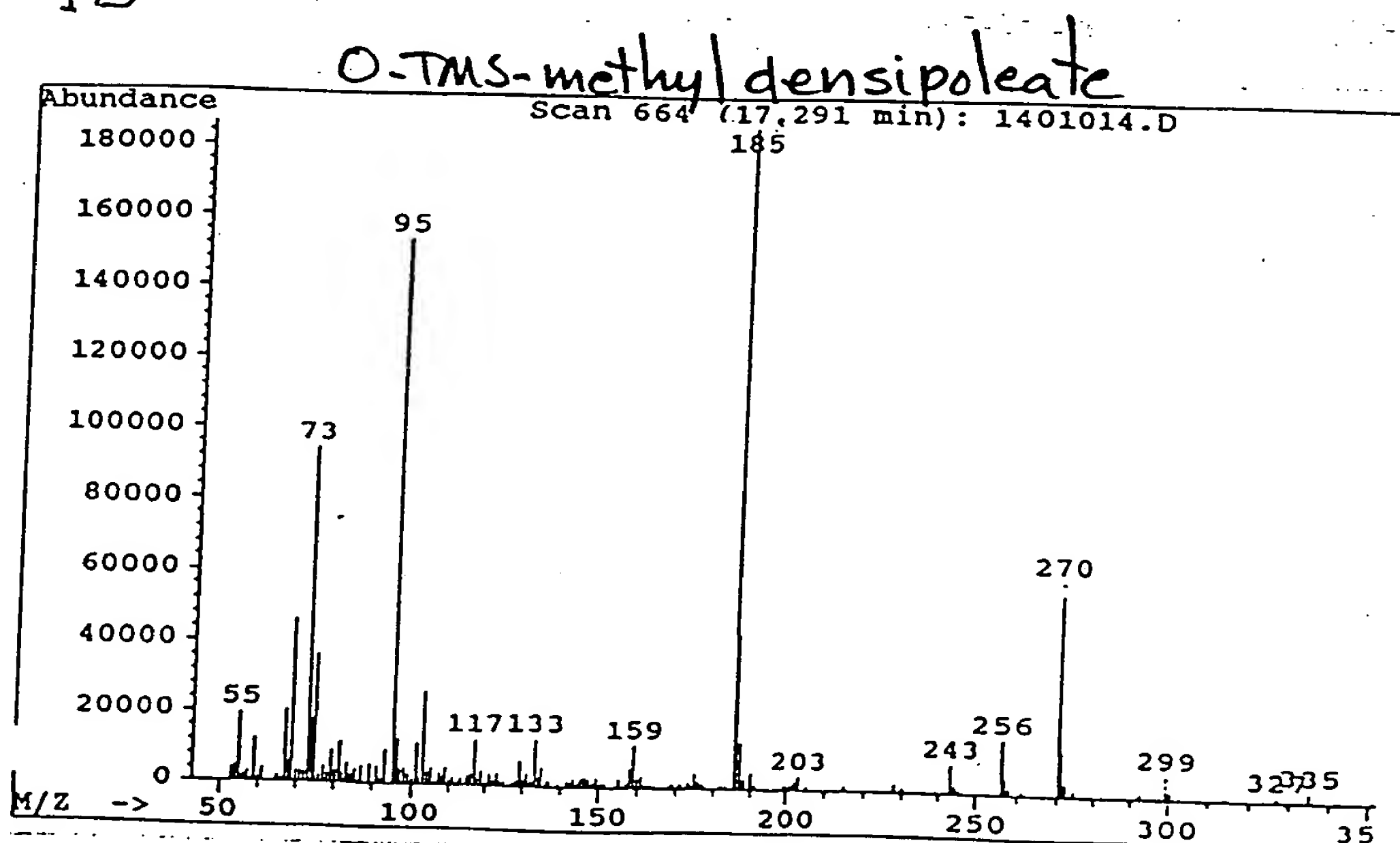


Figure

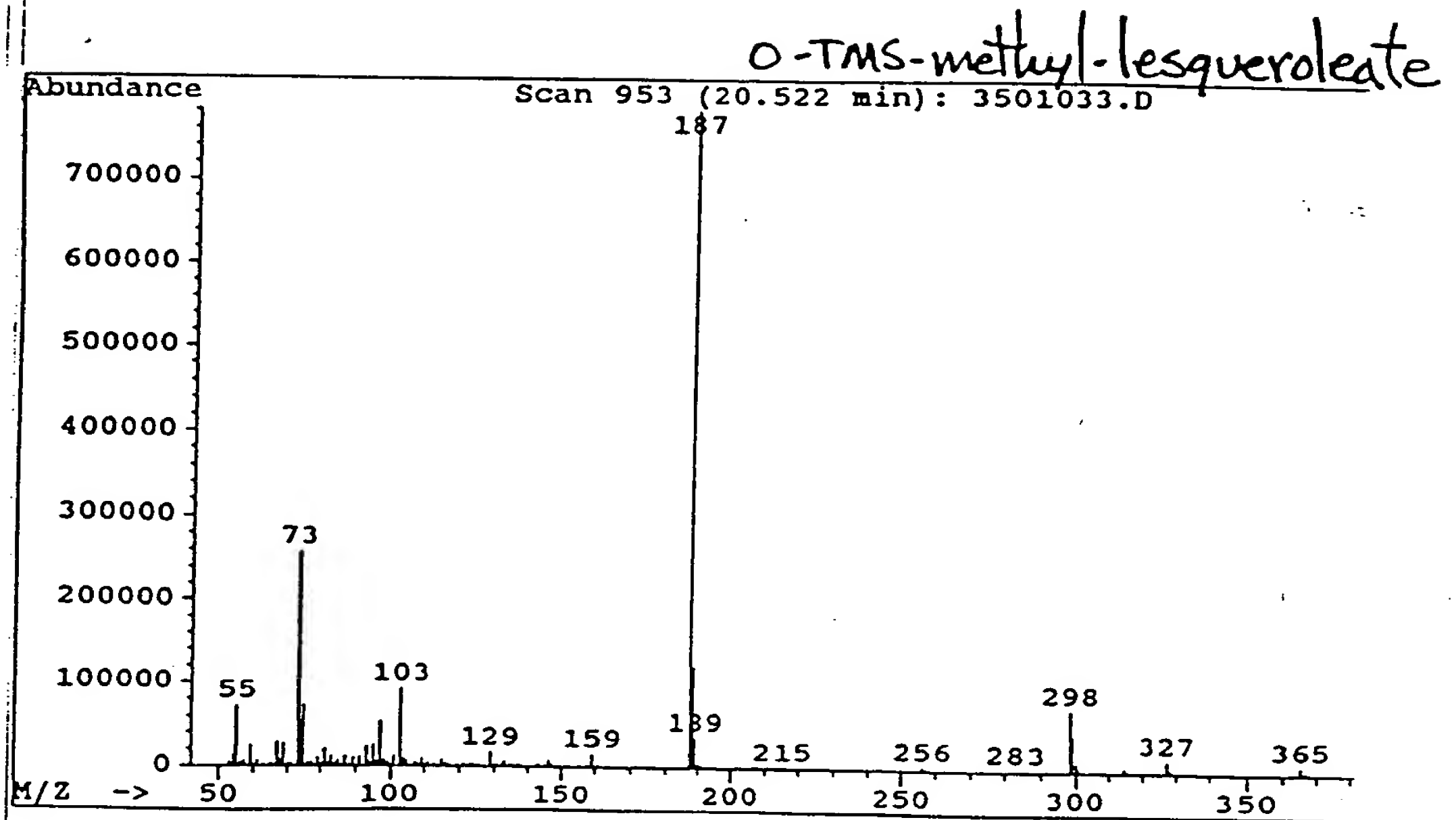
1A



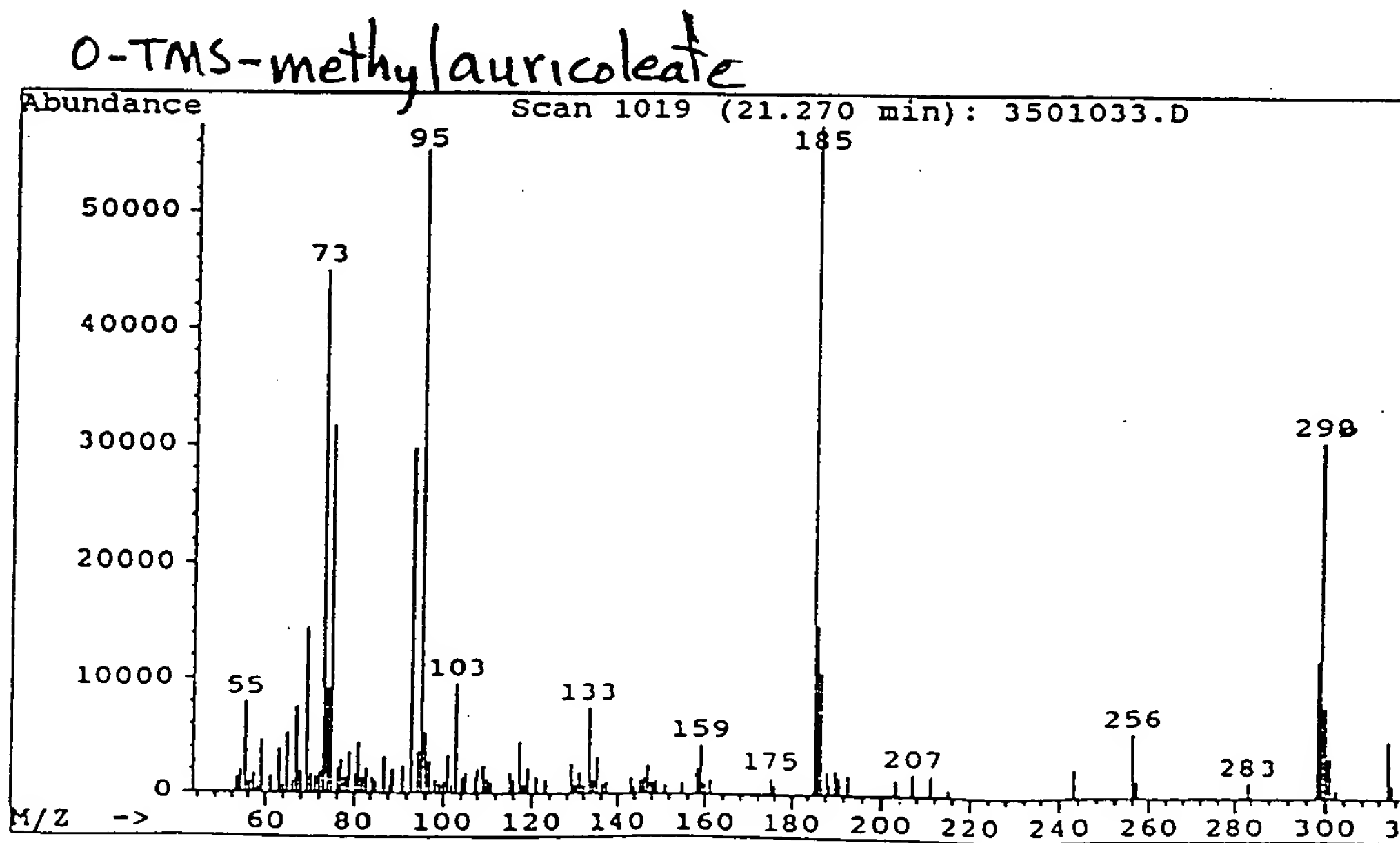
1B



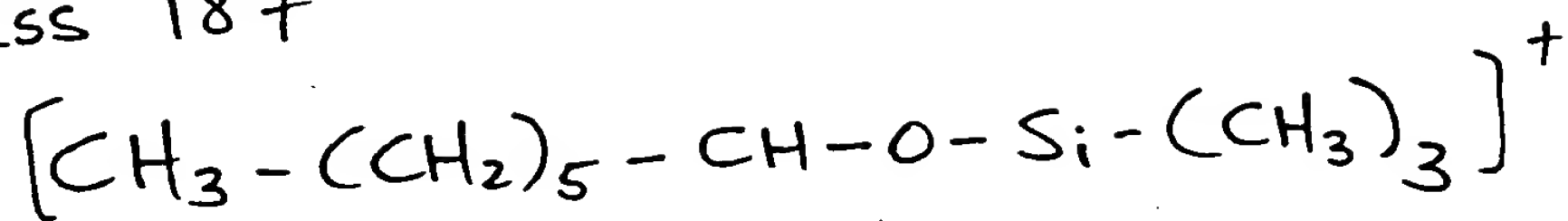
1C



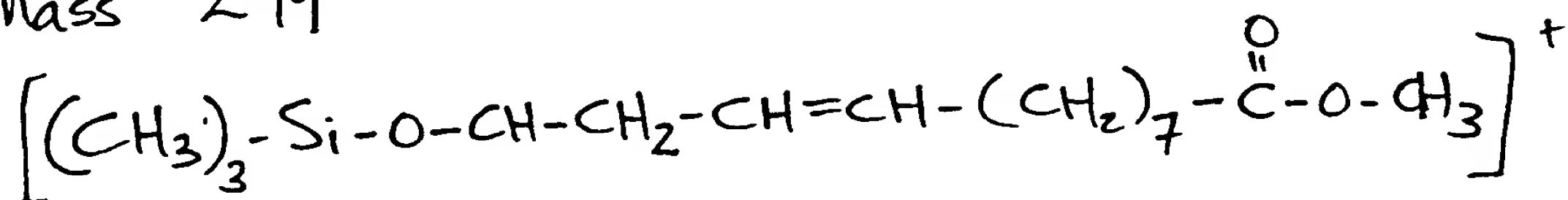
1D



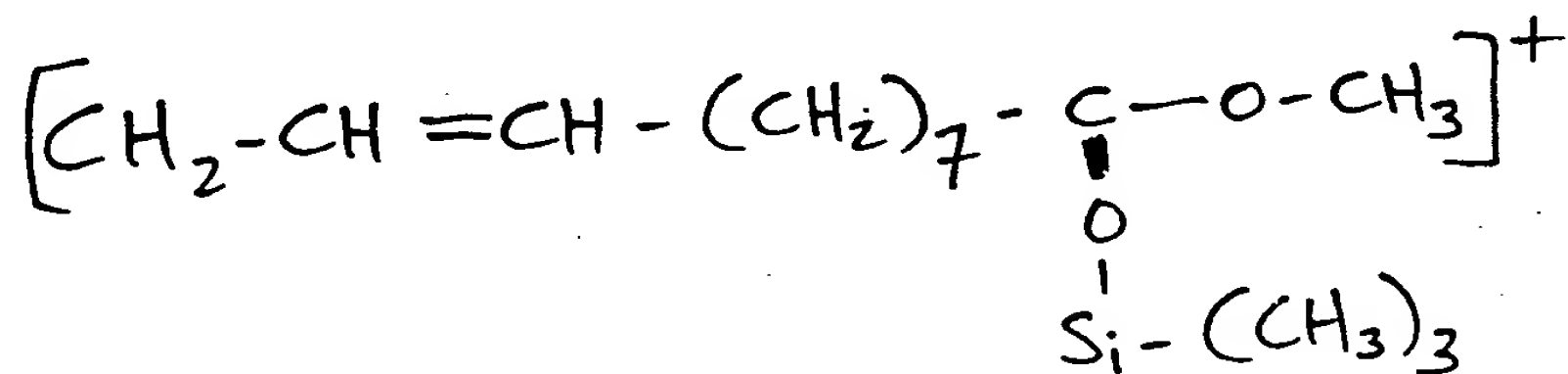
Ion #1: Mass 187



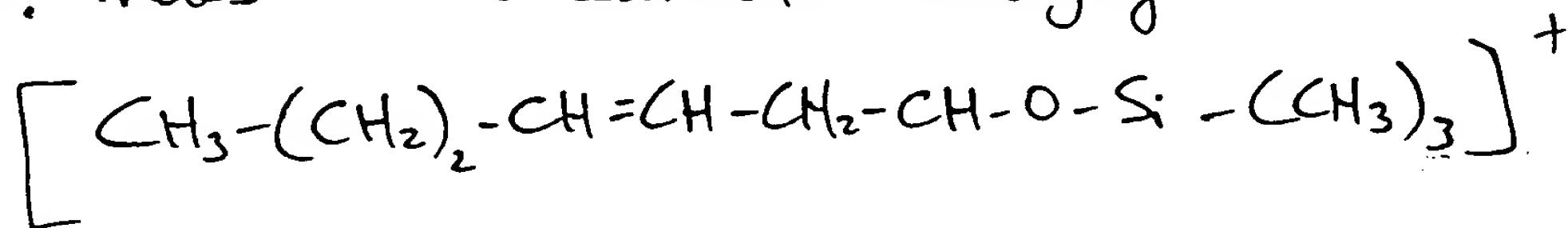
Ion #2: Mass 299



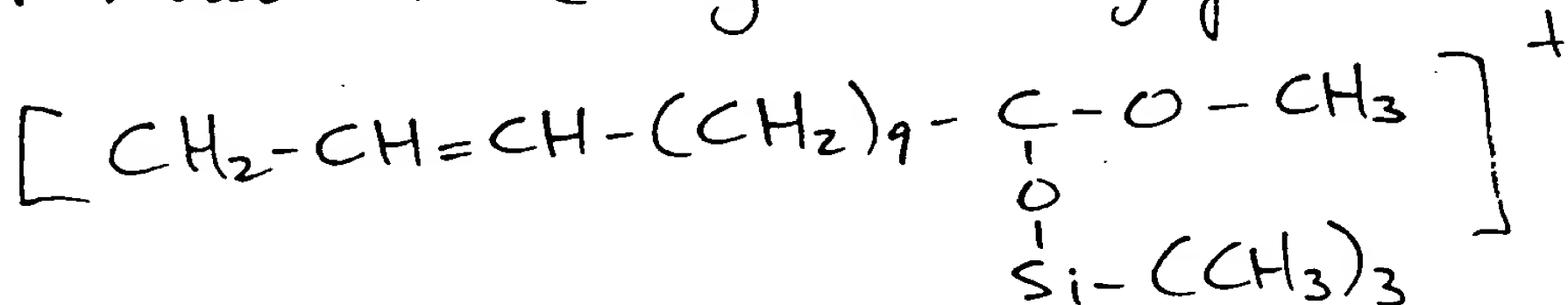
Ion #3: Mass 270 (characteristic rearrangement ion)



Ion #4: Mass 185 (desaturated analog of Ion #1)



Ion #5: Mass 298 (elongated analog of Ion #3)



Ion #6: Mass 327 (elongated analog of Ion #2)

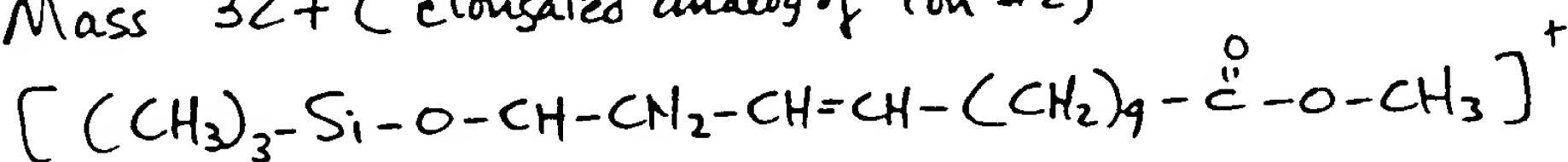


Figure 2.

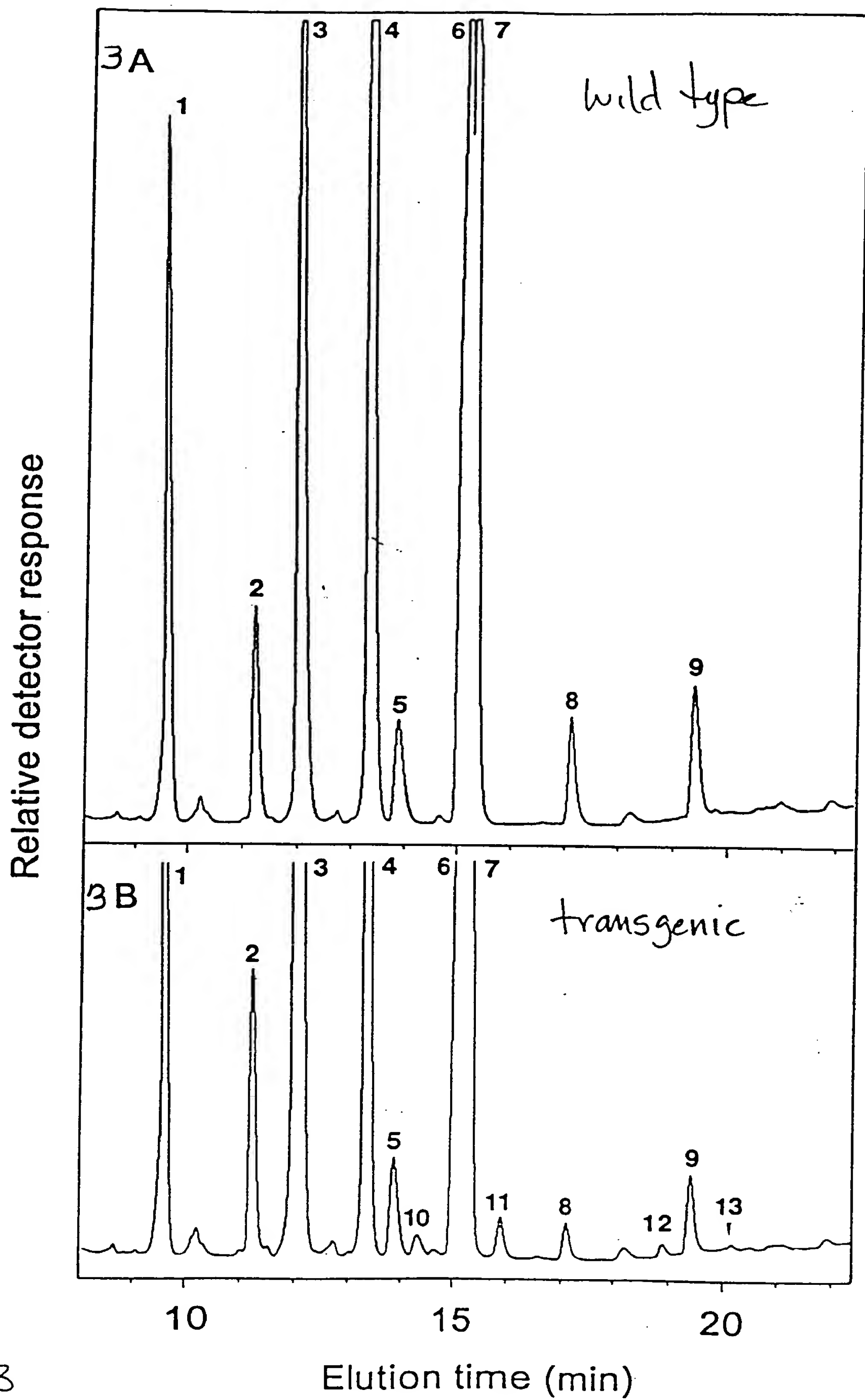
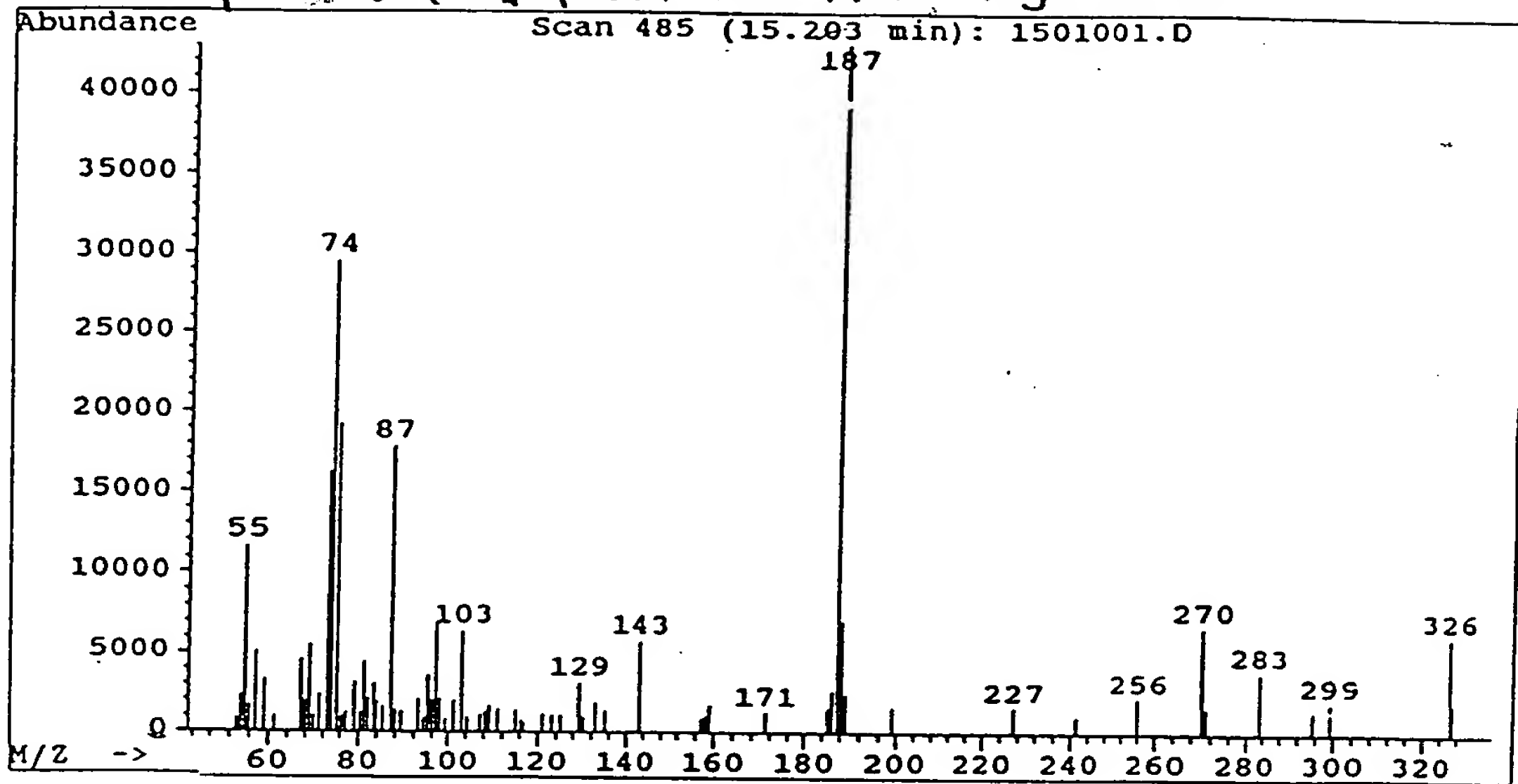


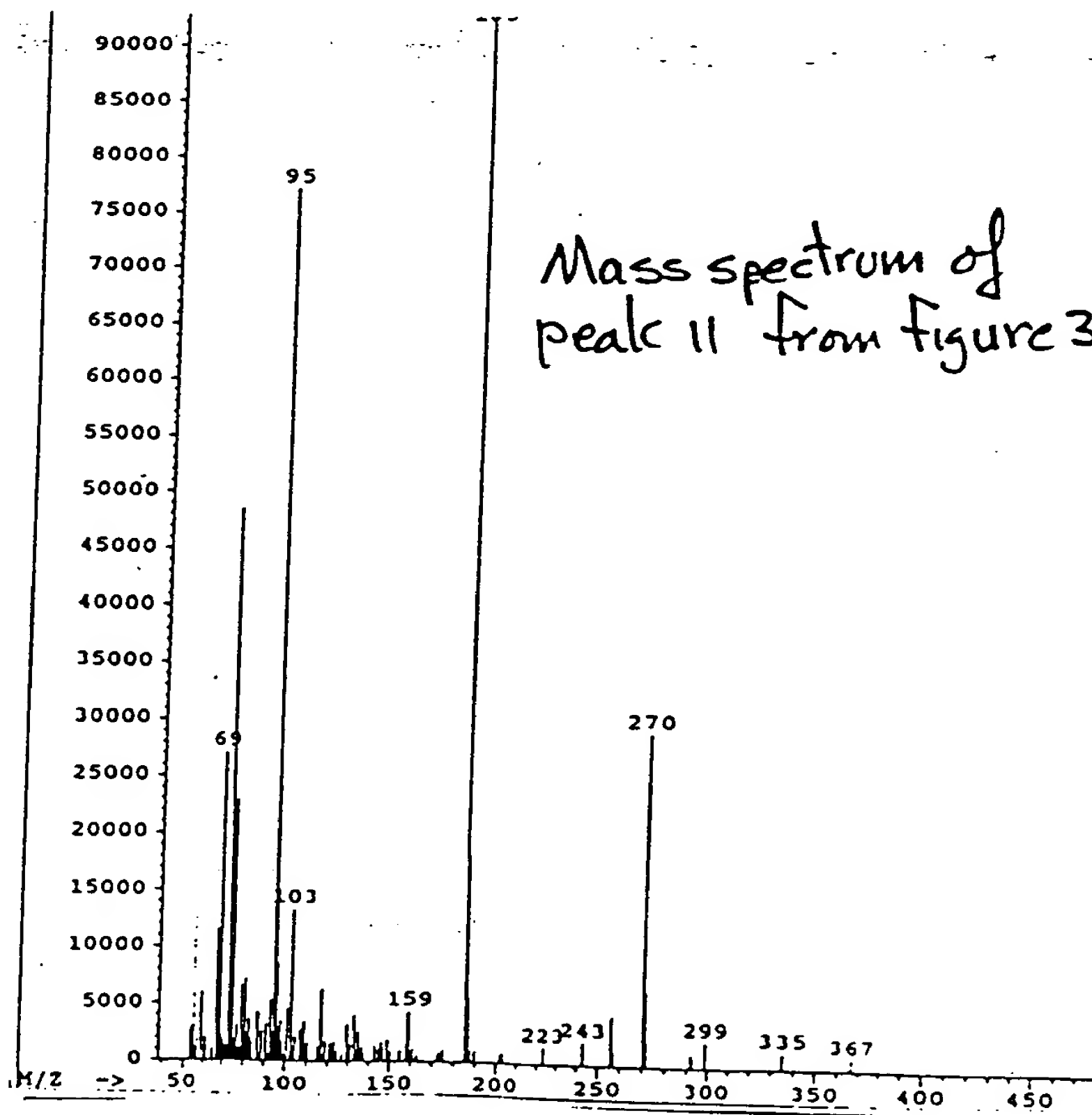
Figure 3

Figure  
4A.

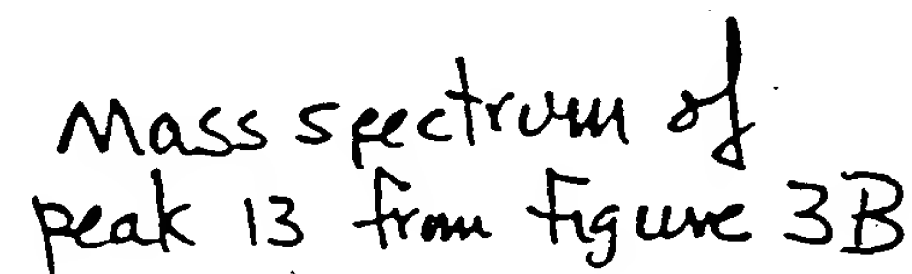
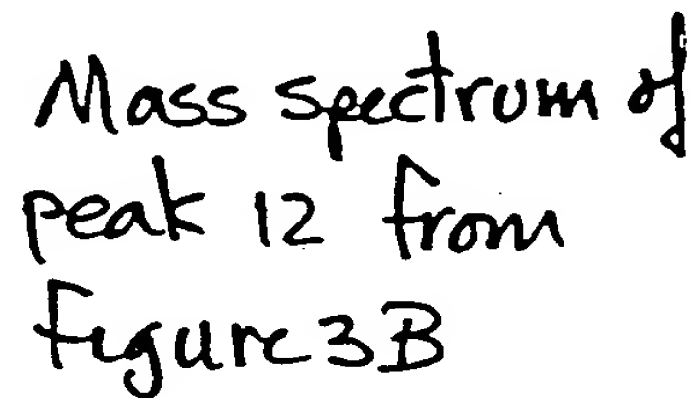
Mass Spectrum of peak 10 from Figure 3B



4B



Year	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	



10	20	30	40	50	60
TATTGGCACC	GGCGGCACCA	TTCCAACAAT	GGATCCCTAG	AAAAAGATGA	AGTCTTTGTC
70	80	90	100	110	120
CCACCTAAGA	AAGCTGCAGT	CANATGGTAT	GTCAAATACC	TCAACAACCC	TCTTGGACGC
130	140	150	160	170	180
ATTCTGGTGT	TAACAGTTCA	GTTTATCCTC	GGGTGGCCTT	TGTATCTAGC	CTTTAATGTA
190	200	210	220	230	240
TCAGGTAGAC	CTTATGATGG	TTTCGCTTCA	CATTTCTTCC	CTCATGCACC	TATCTTTAAG
250	260	270	280	290	300
GACCGTGAAC	GTCTCCAGAT	ATACATCTCA	GATGCTGGTA	TTCTAGCTGT	CTGTTATGGT
310	320	330	340	350	360
CTTTACCGTT	ACGCTGCTTC	ACAAGGATTG	ACTGCTATGA	TCTGCGTCTA	CGGAGTACCG
370	380	390	400	410	420
CTTTTGATAG	TGAACTTTT	CCTTGTCTTG	GTCACCTTCT	TGCAGCACAC	TCATCCTTCA
430	440	450	460	470	480
TTACCTCACT	ATGATTCAAC	CGAGTGGGAA	TGGATTAGAG	GAGCTTTGGT	TACGGTAGAC
490	500	510	520	530	540
AGAGACTATG	GAATCTTGAA	CAAGGTGTTT	CACAACATAA	CAGACACCCA	CGTAGCACAC
550					
CAC					

Figure 5 Nucleotide sequence of pLesq2

10	20	30	40	50	60
TATAGGCACC	GGAGGCACCA	TTCCAACACA	GGATCCCTCG	AAAGAGATGA	AGTATTTGTC
70	80	90	100	110	120
CCAAAGCAGA	AATCCGCAAT	CAAGTGGTAC	GGCGAATACC	TCAACAACCC	TCCTGGTCGC
130	140	150	160	170	180
ATCATGATGT	TAACTGTCCA	GTTCGTCCTC	GGATGGCCCT	TGTACTTAGC	CTTCAACGTT
190	200	210	220	230	240
TCTGGCAGAC	CCTACAATGG	TTTCGCTTCC	CATTTCTTCC	CCAATGCTCC	TATCTACAAC
250	260	270	280	290	300
GACCGTGAAC	GCCTCCAGAT	TTACATCTCT	GATGCTGGTA	TTCTAGCCGT	CTGTTATGGT
310	320	330	340	350	360
CTTTACCGTT	ACGCTGTTGC	ACAAGGACTA	GCCTCAATGA	TCTGTCTAAA	CGGAGTTCCG
370	380	390	400	410	420
CTTCTGATAG	TTAACTTTTT	CCTCGTCTTG	ATCACTTACT	TACAACACAC	TCACCCTGCG
430	440	450	460	470	480
TTGCCTCACT	ATGATTCATC	AGAGTGGGAT	TGGCTTAGAG	GAGCTTTAGC	TACTGTAGAC
490	500	510	520	530	540
AGAGACTATG	GAATCTTGAA	CAAGGTGTTC	CATAACATCA	CAGACACCCA	CGTCGCACAC
550					
CACT					

Figure 6 Nucleotide sequence of pLesq3



0935133-063101

Probe  
pLesq3

S L

Probe  
pLesq2

S L

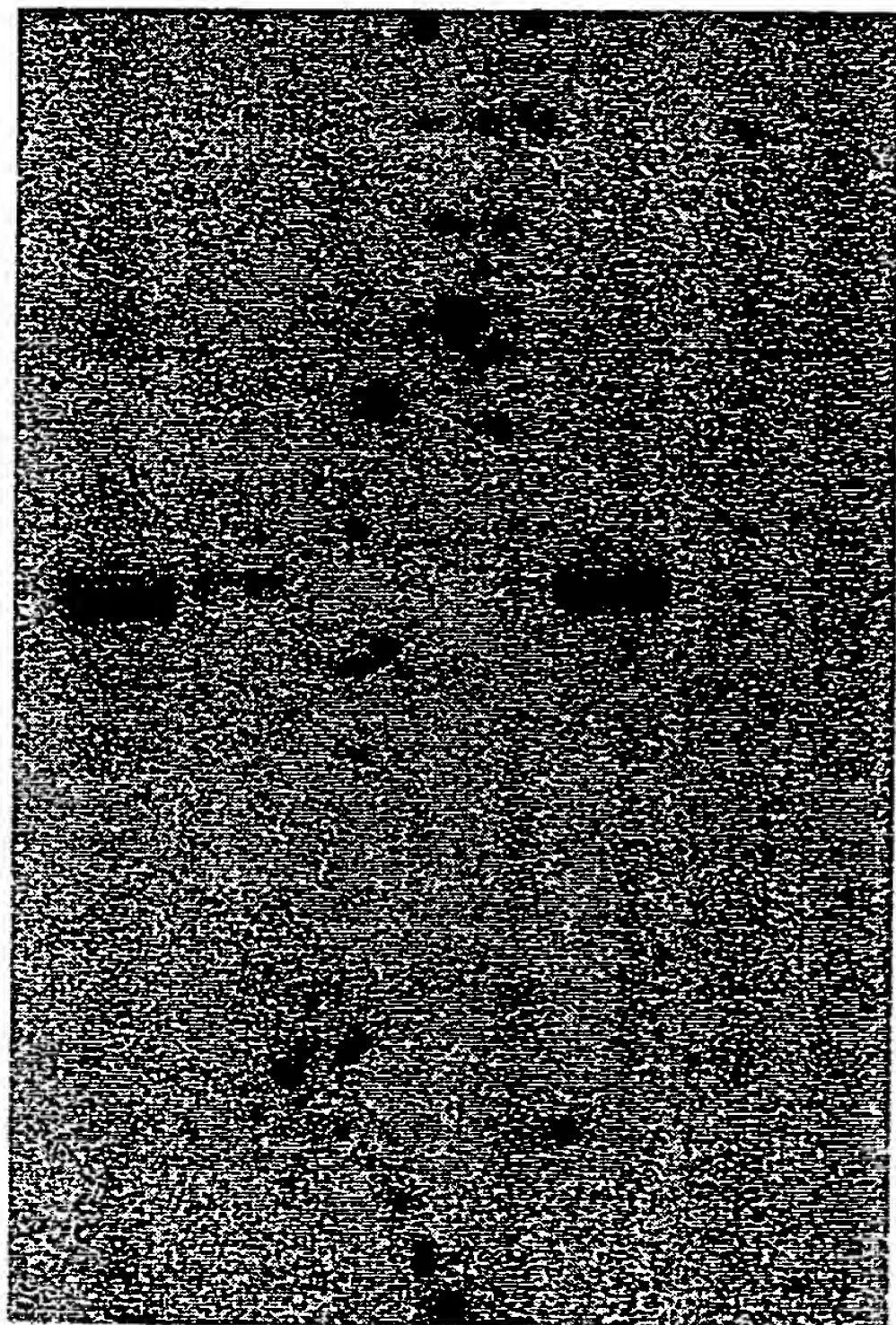


Figure 7

AT	GAA	GCT	TTA	TAA	GAA	GTT	AGT	TTT	CTC	TGG	TGA	CAG	AGA	AAT	TNT	47
GTC	AAT	TGG	TAG	TGA	CAG	TTG	AAG	CAA	CAG	GAA	CAA	CAA	GGA	TGG	TTG	95
GTG	NTG	ATG	CTG	ATG	TGG	TGA	TGT	GTT	ATT	CAT	CAA	ATA	CTA	AAT	ACT	143
ACA	TTA	CTT	GTT	GCT	GCC	TAC	TTC	TCC	TAT	TTC	CTC	CGC	CAC	CCA	TTT	191
TGG	ACC	CAC	GAN	CCT	TCC	ATT	TAA	ACC	CTC	TCT	CGT	GCT	ATT	CAC	CAG	239
AAG	AGA	AGC	CAA	GAG	AGA	GAG	AGA	GAG	AAT	GTT	CTG	AGG	ATC	ATT	GTC	287
TTC	TTC	ATC	GTT	ATT	AAC	GTA	AGT	TTT	TTT	TGA	CCA	CTC	ATA	TCT	AAA	335
ATC	TAG	TAC	ATG	CAA	TAG	ATT	AAT	GAC	TGT	TCC	TTC	TTT	TGA	TAT	TTT	383
						Met	Gly	Ala	Gly	Gly	Arg	Ile	Met	Val	Thr	10
CAG	CTT	CTT	GAA	TTC	AAG	ATG	GGT	GCT	GGT	GGA	AGA	ATA	ATG	GTT	ACC	431
Pro	Ser	Ser	Lys	Lys	Ser	Glu	Thr	Glu	Ala	Leu	Lys	Arg	Gly	Pro	Cys	26
CCC	TCT	TCC	AAG	AAA	TCA	GAA	ACT	GAA	GCC	CTA	AAA	CGT	GGA	CCA	TGT	479
Glu	Lys	Pro	Pro	Phe	Thr	Val	Lys	Asp	Leu	Lys	Lys	Ala	Ile	Pro	Gln	42
GAG	AAA	CCA	CCA	TTC	ACT	GTT	AAA	GAT	CTG	AAG	AAA	GCA	ATC	CCA	CAG	527
His	Cys	Phe	Lys	Arg	Ser	Ile	Pro	Arg	Ser	Phe	Ser	Tyr	Leu	Leu	Thr	58
CAT	TGT	TTC	AAG	CGC	TCT	ATC	CCT	CGT	TCT	TTC	TCC	TAC	CTT	CTC	ACA	575
Asp	Ile	Thr	Leu	Val	Ser	Cys	Phe	Tyr	Tyr	Val	Ala	Thr	Asn	Tyr	Phe	74
GAT	ATC	ACT	TTA	GTT	TCT	TGC	TTC	TAC	TAC	GTT	GCC	ACA	AAT	TAC	TTC	623
Ser	Leu	Leu	Pro	Gln	Pro	Leu	Ser	Thr	Tyr	Leu	Ala	Trp	Pro	Leu	Tyr	90
TCT	CTT	CTT	CCT	CAG	CCT	CTC	TCT	ACT	TAC	CTA	GCT	TGG	CCT	CTC	TAT	671
Trp	Val	Cys	Gln	Gly	Cys	Val	Leu	Thr	Gly	Ile	Trp	Val	Ile	Gly	His	106
TGG	GTA	TGT	CAA	GGC	TGT	GTC	TTA	ACC	GGT	ATC	TGG	GTC	ATT	GGC	CAT	719
Glu	Cys	Gly	His	His	Ala	Phe	Ser	Asp	Tyr	Gln	Trp	Val	Asp	Asp	Thr	122
GAA	TGT	GGT	CAC	CAT	GCA	TTC	AGT	GAC	TAT	CAA	TGG	GTA	GAT	GAC	ACT	767
Val	Gly	Phe	Ile	Phe	His	Ser	Phe	Leu	Leu	Val	Pro	Tyr	Phe	Ser	Trp	138
GTT	GGT	TTT	ATC	TTC	CAT	TCC	TTC	CTT	CTC	GTC	CCT	TAC	TTC	TCC	TGG	815
Lys	Tyr	Ser	His	Arg	Arg	His	His	Ser	Asn	Asn	Gly	Ser	Leu	Glu	Lys	154
AAA	TAC	AGT	CAT	CGT	CGT	CAC	CAT	TCC	AAC	AAT	GGA	TCT	CTC	GAG	AAA	863
Asp	Glu	Val	Phe	Val	Pro	Pro	Lys	Lys	Ala	Ala	Val	Lys	Trp	Tyr	Val	170
GAT	GAA	GTC	TTT	GTC	CCA	CCG	AAG	AAA	GCT	GCA	GTC	AAA	TGG	TAT	GTT	911
Lys	Tyr	Leu	Asn	Asn	Pro	Leu	Gly	Arg	Ile	Leu	Val	Leu	Thr	Val	Gln	186
AAA	TAC	CTC	AAC	AAC	CCT	CTT	GGA	CGC	ATT	CTG	GTG	TTA	ACA	GTT	CAG	959

Figure 8A

Phe	Ile	Leu	Gly	Trp	Pro	Leu	Tyr	Leu	Ala	Phe	Asn	Val	Ser	Gly	Arg	202
TTT	ATC	CTC	GGG	TGG	CCT	TTG	TAT	CTA	GCC	TTT	AAT	GTA	TCA	GGT	AGA	1007
Pro	Tyr	Asp	Gly	Phe	Ala	Ser	His	Phe	Phe	Pro	His	Ala	Pro	Ile	Phe	218
CCT	TAT	GAT	GGT	TTC	GCT	TCA	CAT	TTC	TTC	CCT	CAT	GCA	CCT	ATC	TTT	1055
Lys	Asp	Arg	Glu	Arg	Leu	Gln	Ile	Tyr	Ile	Ser	Asp	Ala	Gly	Ile	Leu	234
AAA	GAC	CGA	GAA	CGC	CTC	CAG	ATA	TAC	ATC	TCA	GAT	GCT	GGT	ATT	CTA	1103
Ala	Val	Cys	Tyr	Gly	Leu	Tyr	Arg	Tyr	Ala	Ala	Ser	Gln	Gly	Leu	Thr	250
GCT	GTC	TGT	TAT	GGT	CTT	TAC	CGT	TAC	GCT	GCT	TCA	CAA	GGA	TTG	ACT	1151
Ala	Met	Ile	Cys	Val	Tyr	Gly	Val	Pro	Leu	Leu	Ile	Val	Asn	Phe	Phe	266
GCT	ATG	ATC	TGC	GTC	TAT	GGA	GTA	CCG	CTT	TTG	ATA	GTG	AAC	TTT	TTC	1199
Leu	Val	Leu	Val	Thr	Phe	Leu	Gln	His	Thr	His	Pro	Ser	Leu	Pro	His	282
CTT	GTC	TTG	GTA	ACT	TTC	TTG	CAG	CAC	ACT	CAT	CCT	TCG	TTA	CCT	CAT	1247
Tyr	Asp	Ser	Thr	Glu	Trp	Glu	Trp	Ile	Arg	Gly	Ala	Leu	Val	Thr	Val	298
TAT	GAT	TCA	ACC	GAG	TGG	GAA	TGG	ATT	AGA	GGA	GCT	TTG	GTT	ACG	GTA	1295
Asp	Arg	Asp	Tyr	Gly	Ile	Leu	Asn	Lys	Val	Phe	His	Asn	Ile	Thr	Asp	314
GAC	AGA	GAC	TAT	GGA	ATA	TTG	AAC	AAG	GTG	TTC	CAT	AAC	ATA	ACA	GAC	1343
Thr	His	Val	Ala	His	His	Leu	Phe	Ala	Thr	Ile	Pro	His	Tyr	Asn	Ala	330
ACA	CAT	GTG	GCT	CAT	CAT	CTC	TTT	GCA	ACT	ATA	CCG	CAT	TAT	AAC	GCA	1391
Met	Glu	Ala	Thr	Glu	Ala	Ile	Lys	Pro	Ile	Leu	Gly	Asp	Tyr	Tyr	His	346
ATG	GAA	GCT	ACA	GAG	GCG	ATA	AAG	CCA	ATA	CTT	GGT	GAT	TAC	TAC	CAC	1439
Phe	Asp	Gly	Thr	Pro	Trp	Tyr	Val	Ala	Met	Tyr	Arg	Glu	Ala	Lys	Glu	362
TTC	GAT	GGA	ACA	CCG	TGG	TAT	GTG	GCC	ATG	TAT	AGG	GAA	GCA	AAG	GAG	1487
Cys	Leu	Tyr	Val	Glu	Pro	Asp	Thr	Glu	Arg	Gly	Lys	Lys	Gly	Val	Tyr	378
TGT	CTC	TAT	GTA	GAA	CCG	GAT	ACG	GAA	CGT	GGG	AAG	AAA	GGT	GTC	TAC	1535
Tyr	Tyr	Asn	Asn	Lys	Leu											384
TAT	TAC	AAC	AAT	AAG	TTA	TGA	GGC	TGA	TAG	GGC	GAG	AGA	AGT	GCA	ATT	1583
ATC	AAT	CTT	CAT	TTC	CAT	GTT	TTA	GGT	GTC	TTG	TTT	AAG	AAG	CTA	TGC	1631
TTT	GTT	TCA	ATA	ATC	TCA	GAG	TCC	ATN	TAG	TTG	TGT	TCT	GGT	GCA	TTT	1679
TGC	CTA	GTT	ATG	TGG	TGT	CGG	AAG	TTA	GTG	TTC	AAA	CTG	CTT	CCT	GCT	1727
GTG	CTG	CCC	AGT	GAA	GAA	CAA	GTT	TAC	GTG	TTT	AAA	ATA	CTC	GGA	ACG	1775
AAT	TGA	CCA	CAA	NAT	ATC	CAA	AAC	CGG	CTA	TCC	GAA	TTC	CAT	ATC	CGA	1823
AAA	CCG	GAT	ATC	CAA	ATT	TCC	AGA	GTA	CTT	AG						1855

Figure 8B

	10	20	30	40	50	
LFFAH12.AMI	1	MGAGGRIM-- --VTPSSKKS	--ETEALKRG	PCEKPPFTVK	DLKKAIPQHC	
FAH12.AMI	1	MGGGGRMSTV	ITSNNSEKKG	--GSSHLKRA	PHTKPPFTLG	DLKRAIPPHC 50
ATFAD2.AMI	1	MGAGGRMP-- --VPTSSKKS	--ETDITTKRV	PCEKPPFSVG	DLKKAIPPHC	50
BNFAD2.AMI	1	MGAGGRMQ-- --VSPPSKKS	--ETDNIKRV	PCETPPFTVG	ELKKAIPPHC	50
AD2-1.AMI	1	MGLA-KETTM	GGRGRVAKVE	VQGKKPLSRV	PNTKPPFTVG	QLKKAIPPHC 50
GMFAD2-2.AMI	1	MGAGGR----	TDVPPANRKS	--EVDPLKRV	PFEKPQFSLS	QIKKAIPPHC 50
ZMFAD2.AMI	1	MGAGGRMTEK	EREKQEQLAR	ATGGAAMQRS	PVEKPPFTLG	QIKKAIPPHC 50
RCFAD2.AMI	1	-----	-----	-----	-----	50
	60	70	80	90	100	
LFFAH12.AMI	51	FKRSIPRSFS	YLLTDITLVS	CFYYVATNYF	SLLPQPLSTY	LAWPLYWVCQ 100
FAH12.AMI	51	FERSFVRSFS	YVAYDVCLSF	LFYSIATNFF	PYISSPLS-Y	VAWLVIWLFQ 100
ATFAD2.AMI	51	FKRSIPRSFS	YLISDIIIAS	CFYYVATNYF	SLLPQPLS-Y	LAWPLYWACQ 100
BNFAD2.AMI	51	FKRSIPRSFS	HLIWDIIIAS	CFYYVATTYF	PLLPNPLS-Y	FAWPLYWACQ 100
GMFAD2-1.AMI	51	FQRSLLTSFS	YVVYDLSEAF	IFY-IATTYF	HLLPQPFS-L	IAWPIYWVLQ 100
GMFAD2-2.AMI	51	FQRSVLRFSFS	YVVYDLTIAF	CLYYVATHYF	HLLPGPLS-F	RGMAIYWAVQ 100
ZMFAD2.AMI	51	FERSVLKSFS	YVVHDLVIAA	ALLYFALAI	PALPSPLR-Y	AAWPLYWIAQ 100
RCFAD2.AMI	51	-----	-----	-----	-----	100
	110	120	130	140	150	
LFFAH12.AMI	101	GCVLTGIWVI	GHECGHHAFS	DYQWVDDTVG	FIFHSFLLVP	YFSWKYSHRR 150
FAH12.AMI	101	GCILTGLWVI	GHECGHHAFS	EYQLADDIVG	LIVHSALLVP	YFSWKYSHRR 150
ATFAD2.AMI	101	GCVLTGIWVI	AHECGHHAFS	DYQWLDDTVG	LIFHSFLLVP	YFSWKYSHRR 150
BNFAD2.AMI	101	GCVLTGVWVI	AHECGHAAFS	DYQWLDDTVG	LIFHSFLLVP	YFSWKYSHRR 150
GMFAD2-1.AMI	101	GCLLTGVWVI	AHECGHHAFS	KYQWVDDVVG	LTLHSTLLVP	YFSWKISHRR 150
GMFAD2-2.AMI	101	GCILTGVWVI	AHECGHHAFS	DYQLLDDIVG	LILHSALLVP	YFSWKYSHRR 150
ZMFAD2.AMI	101	G-----	-----AFS	DYSLDDVVG	LVLHSSLMVP	YFSWKYSHRR 150
RCFAD2.AMI	101	-----WVM	AHDCGHHAFS	DYQLLDDVVG	LILHSCLLVP	YFSWKHSHRR 150
	160	170	180	190	200	
LFFAH12.AMI	151	HHSNIGSLEK	DEVFVPPKKA	AVKWYVKYL-	NNPLGRILVL	TVQFILGWPL 200
FAH12.AMI	151	HHSNIGSLER	DEVFVPKSKS	KISWYSKYS-	NNPPGRVLT	AATLLLGWPL 200
ATFAD2.AMI	151	HHSNIGSLER	DEVFVPKQKS	AIKWYGKYL-	NNPLGRIMML	TVQFVLGWPL 200
BNFAD2.AMI	151	HHSNIGSLER	DEVFVPR-RS	QTSSGTAST-	STTFGRVML	TVQFTLGWPL 200
GMFAD2-1.AMI	151	HHSNIGSLDR	DEVFVPKPKS	KVAWFSKYL-	NNPLGRAVSL	LVTLTIGWPM 200
GMFAD2-2.AMI	151	HHSNIGSLER	DEVFVPKQKS	CIKWYSKYL-	NNPPGRVLT	AVTLTLGWPL 200
ZMFAD2.AMI	151	HHSNIGSLER	DEVFVPKKKE	ALPWYTPYVY	NNPVGRVVHI	VVQLTLGWPL 200
RCFAD2.AMI	151	HHSNIGSLER	DEVFVPKKKS	SIRWYSKYL-	NNPPGRIMTI	AVTLSLGWPL 200
	210	220	230	240	250	
LFFAH12.AMI	201	YLAFNVSGRP	YDG-FASHFF	PHAPIFKDRE	RLQIYISDAG	ILAVCYGLYR 250
FAH12.AMI	201	YLAFNVSGRP	YDR-FACHYD	PYGPIFSERE	RLQIYIADLG	IFATTFVLYQ 250
ATFAD2.AMI	201	YLAFNVSGRP	YDG-FACHFF	PNAPIYNDRE	RLQIYLSDAG	ILAVCFGLYR 250
BNFAD2.AMI	201	YLAFNVSGRP	YDGGFACHFH	PNAPIYNDRE	RLQIYISDAG	ILAVCYGLLP 250
GMFAD2-1.AMI	201	YLAFNVSGRP	YDS-FASHYH	PYAPIYSNRE	RLLIYVSDVA	LFSVTYSLYR 250
GMFAD2-2.AMI	201	YLALNVSGRP	YDR-FACHYD	PYGPIYSDRE	RLQIYISDAG	VLAVVYGLFR 250
ZMFAD2.AMI	201	YLATNASGRP	YPR-FACHFD	PYGPIYNDRE	RAQIFVSDAG	VVAVAFGLYK 250
RCFAD2.AMI	201	YLAFNVSGRP	YDR-FACHYD	PYGPIYNDRE	RIEIFISDAG	VLAVTFGLYQ 250
	260	270	280	290	300	
LFFAH12.AMI	251	YAASQGLTAM	ICVYGVPLLI	VNFFLVLTTF	LQHTHPSLPH	YDSTEWELIR 300
FAH12.AMI	251	ATMAKGLAWV	MRIYGVPLLI	VNCFLVMITY	LQHTHPAIPR	YGSSEWDWLR 300
ATFAD2.AMI	251	YAAAQGMASM	ICLYGVPLLI	VNAFLVLITY	LQHTHPSLPH	YDSSEWDWLR 300
BNFAD2.AMI	251	YAAVQGVASM	VCFLRVPLLI	VNGFLVLITY	LQHTHPSLPH	YDSSEWDWLR 300
GMFAD2-1.AMI	251	VATLKGLVWL	LCVYGVPLLI	VNGFLVTITY	LQHTHFALPH	YDSSEWDWLK 300
AD2-2.AMI	251	LAMAKGLAWV	VCVYGVPLLV	VNGFLVLITF	LQHTHPALPH	YTSSEWDWLR 300
ZMFAD2.AMI	251	LAAAFGVWVW	VRVYAVPLLI	VNAWLVLITY	LQHTHPSLPH	YDSSEWDWLR 300

Figure 9A

RCFAD2.AMI	251	LATAKGLAWV	VCVYGVPLL	VNSFLVLITF	LQHTHPALPH	YDSSEWDWLR	300
		310	320	330	340	350	
LFFAH12.AMI	301	GALVTVDRDY	GILNKVFHNI	TDTHVAHHLF	ATIPHYNAME	ATEAIKPILG	350
FAH12.AMI	301	GAMVTVDRDY	GVLNKVFHNI	ADTHVAHHLF	ATVPHYHAME	ATKAIKPIMG	350
AD2.AMI	301	GALATVDRDY	GILNKVFHNI	TDTHVAHHLF	STMPHYNAME	ATKAIKPILG	350
BNFAD2.AMI	301	GALATVDRDY	GILNQGFHNI	TDTHEAHHLF	STMPHYHAME	ATKAIKPILG	350
GMFAD2-1.AMI	301	GALATMDRDY	GILNKVFHHI	TDTHVAHHLF	STMPHYHAME	ATNAIKPILG	350
GMFAD2-2.AMI	301	GALATVDRDY	GILNKVFHNI	TDTHVAHHLF	STMPHYHAME	ATKAIKPILG	350
ZMFAD2.AMI	301	GALATMDRDY	GILNRVFHNI	TDTHVAHHLF	STMPHYHAME	ATKAIRPILG	350
RCFAD2.AMI	301	GALATVDRDY	GILNKVFHNI	TDTHVAHHLF	-TMP-----	-----	350
		360	370	380	390	400	
LFFAH12.AMI	351	DYYHFDGTPW	YVAMYREAKE	CLYVEPDTER	GKKGVYYYNN	K-L.....	400
FAH12.AMI	351	EYYRYDGTPTF	YKALWREAKE	CLFVEPDEGA	PTQGVFWYRN	KY-.....	400
ATFAD2.AMI	351	DYYQFDGTPW	YVAMYREAKE	CIYVEPDREG	DKKGVWYNN	K-L.....	400
BNFAD2.AMI	351	EYYQFDGTPV	VKAMWREAKE	CIYVEPDROG	EKKGVFWYNN	KL*.....	400
GMFAD2-1.AMI	351	EYYQFDGTPF	YKALWREARE	CLYVEPDDEGT	SEKGVWYNN	KY-.....	400
GMFAD2-2.AMI	351	EYYRFDETPF	VKAMWREARE	CIYVEPDQST	ESKGVFWYNN	KL-.....	400
ZMFAD2.AMI	351	DYYHFDPTPV	AKATWREAGE	CIYVEPE---	DRKGVFWYNK	KF*.....	400
RCFAD2.AMI	351	-----	-----	-----	-----	-----	400
		410	420	430	440	450	
LFFAH12.AMI	401	.....	.....	.....	.....	.....	450
FAH12.AMI	401	.....	.....	.....	.....	.....	450
ATFAD2.AMI	401	.....	.....	.....	.....	.....	450
BNFAD2.AMI	401	.....	.....	.....	.....	.....	450
GMFAD2-1.AMI	401	.....	.....	.....	.....	.....	450
GMFAD2-2.AMI	401	.....	.....	.....	.....	.....	450
ZMFAD2.AMI	401	.....	.....	.....	.....	.....	450

Figure 9B



0989499-06404  
TOT290-88T9860

Molecular weight markers



E H X

3.6 -

1.8 -

1.5 -

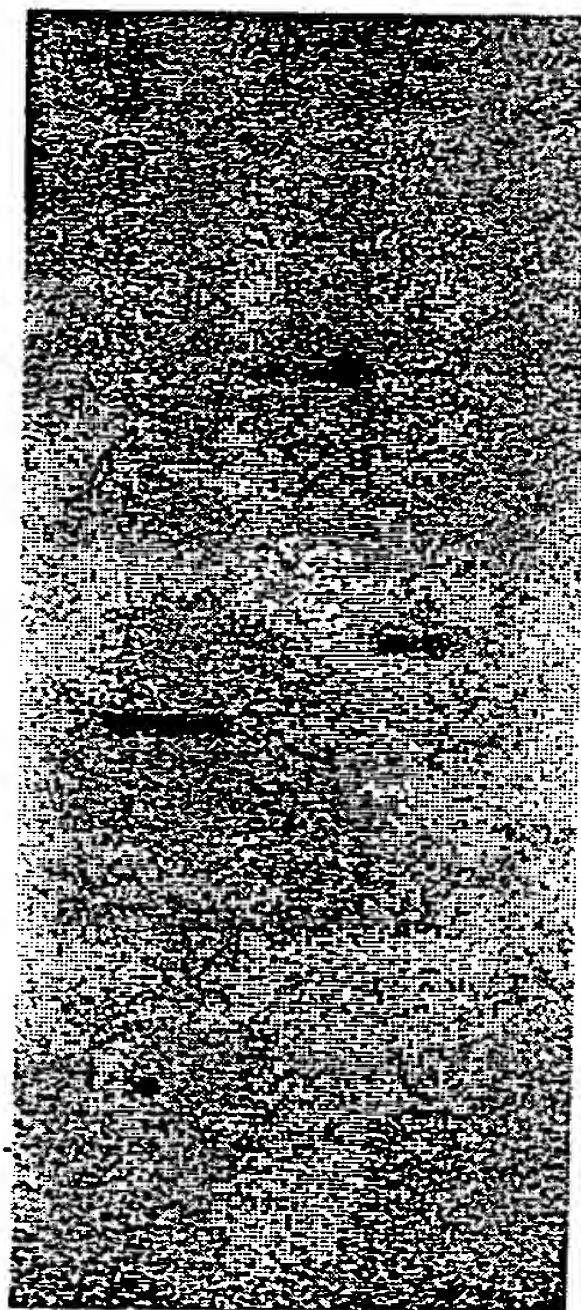


Figure 10

	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99
00000	00001	00002	00003	00004	00005	00006	00007	00008	00009	00010	00011	00012	00013	00014	00015	00016	00017	00018	00019	00020	00021	00022	00023	00024	00025	00026	00027	00028	00029	00030	00031	00032	00033	00034	00035	00036	00037	00038	00039	00040	00041	00042	00043	00044	00045	00046	00047	00048	00049	00050	00051	00052	00053	00054	00055	00056	00057	00058	00059	00060	00061	00062	00063	00064	00065	00066	00067	00068	00069	00070	00071	00072	00073	00074	00075	00076	00077	00078	00079	00080	00081	00082	00083	00084	00085	00086	00087	00088	00089	00090	00091	00092	00093	00094	00095	00096	00097	00098	00099	

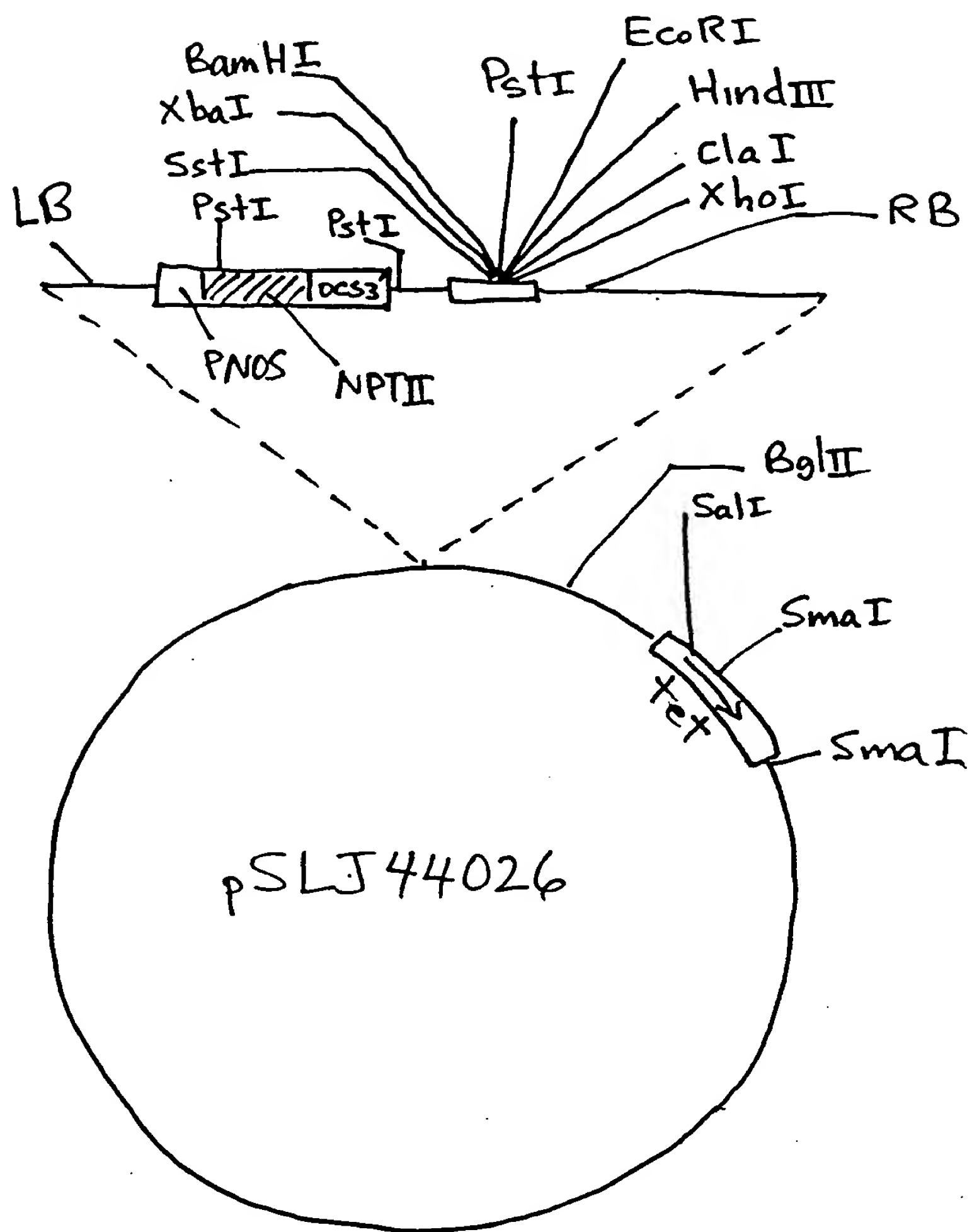


Figure 11